

OIPE

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/847,960

TIME: 11:16:04

Input Set : A:\ES.txt

Output Set: N:\CRF3\09102001\I847960.raw

ENTERED

3 <110> APPLICANT: Swift, Susan E.
4 Bogenberger, Jakob M.
6 <120> TITLE OF INVENTION: RNase PROBE PROTECTION ASSAYS IN SCREENING FOR MODULATORS OF
7 IMMUNOGLOBULIN GERMLINE TRANSCRIPTION
9 <130> FILE REFERENCE: A-69332-1/RMS/JJD
11 <140> CURRENT APPLICATION NUMBER: US 09/847,960
12 <141> CURRENT FILING DATE: 2001-05-02
14 <150> PRIOR APPLICATION NUMBER: US 60/201,333
15 <151> PRIOR FILING DATE: 2000-05-02
17 <160> NUMBER OF SEQ ID NOS: 24
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 533
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial sequence ✓
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Germline Ig Alpha-2 probe ✓
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32 acagcagccc tcttggcagg cagccagacg cccgtgaggg tggacctgcc atgagggcct 120
34 gcacgccgga ggccgcccac tcagcactgc gggccctcca gcagcctgac cagcatcccc 180
36 gaccagcccc aaggtcttcc cgtgagcct cgacagcacc cccaagatg ggaacgtggt 240
38 cgtcgcatgc ctggtccagg gcttcttccc ccaggagcca ctcagtgtga cctggagcga 300
40 aagcggacag aacgtgaccg ccagaaactt cccacctagc caggatgcct ccggggacct 360
42 gtacaccacg agcagccagc tgacctgcc ggccacacag tgcccagacg gcaagtccgt 420
44 gacatgccac gtgaagcact acacgaatcc cagccaggat gtgactgtgc cctgcccagt 480
46 tccccccact ccccatatgt gccacccccg actgtcgtg caccgaccgg ccc 533
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 202
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial sequence ✓
54 <220> FEATURE:
55 <223> OTHER INFORMATION: Germline Ig Epsilon Probe ✓
57 <400> SEQUENCE: 2
58 ggctccactg cccggcacag aaataacaac caccggttact gatcatctgg gagctgtcca 60
60 ggaacccgac agggagccgg acggggccaca ccattccacg gcaccaaag gacgaccgg 120
62 cgcttcagcc tccacacaga gcccatccgt ctcccccttg acccgtgct gcaaaaacat 180
64 tccctccaat gccacctcgg tg 202
67 <210> SEQ ID NO: 3
68 <211> LENGTH: 594
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial sequence ✓
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Germline Ig Gamma 1 probe ✓
75 <400> SEQUENCE: 3
76 acacaccaga ggctgactga ggccctccagg acgaccgggc tgggagcacg aggaacatga 60
78 ctggatgcgg cagagccggc cgtgggggtga tgccaggatg ggcacgaccg acctgagctc 120

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80 aggaggcagc agagcgaggg aggaggagag gccccaggtg aacggagggg cttgtccagg 180
82 ccggcagcat caccggagcc cagggcaggg tcagcagtgc tggccgtggg gccctcctct 240
84 cagccaggac caaggacagc agcctccacc aaggggcccat cggctctccc cctggcacc 300
86 tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 360
88 cccgaaccgg tgacggtgtc gtggaactca ggcgcctga ccagcggcgt gcacaccttc 420
90 ccggtgttcc tacagtcttc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 480
92 agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 540
94 gtggacaaga aagttgagcc caaatcttgt gacaaaactc acacatgccc accg 594
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98 <211> LENGTH: 632
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial sequence ✓
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Germline Ig Gamma 2 probe ✓
105 <400> SEQUENCE: 4
106 ccaagccaac agggcaggac acaccagagg ctgactgagg cctccatgac gaccaggctg 60
108 ggagcacgag gaacatgacg ggatgcgga gagccggcg tggggtgatg ccagcatggg 120
110 caggaccac ctgagctgag gaggcagtag aacgagggag gaggagaggc cccaggtgaa 180
112 cggaggggct tgtccaggcc agcagcatca ctggagccca gggcagggtc agcagtgtg 240
114 gccgtggggc cctctctcag ccaggacca ggacagcagc ctccaccaag ggcccatcgg 300
116 tcttccccct ggcgcctgc tccaggagca cctccgagag cacagcggcc ctgggctgcc 360
118 tggtaagga ctacttcccc gaaccgggtga cgggtgtcgt gaactcaggc gctctgacca 420
120 gcggcgtgca cacttcccc gctgtcctac agtcctcagg actctactcc ctacgagcg 480
122 tggtagcgt gccctccagc aacttcggca cccagacct cacttgcaac gtagatcaca 540
124 agcccagcaa caccaagggtg gacaagacag ttgagcgcaa atgttgtgtc gagtgccac 600
126 cgtgccagc accacctgtg gcaggaccgt ca 632
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130 <211> LENGTH: 650
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial sequence ✓
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Germline Ig Gamma 3 probe ✓
137 <400> SEQUENCE: 5
138 acacaccaga ggctgactga ggctccagg acgaccgggc tgggagcgtg aggaacatga 60
140 cgggatgggg cagagccagc catggggtga tgccaggatg ggcatgaccg acctgagctc 120
142 aggaggcagc agagagaggg aggaggagag gccccaggtg aaccgagggg cttgtccagg 180
144 ccggcagcat caccggagcc cagggcaggg tcagcagagc tggccgtagg gccctcctct 240
146 cagccaggac caaggacagc agcttccacc aaggggccat cggctctccc cctggcgccc 300
148 tgctccagga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc 360
150 cccgaaccgg tgacggtgtc gtggaactca ggcgcctga ccagcggcgt gcacaccttc 420
152 ccggtgttcc tacagtcttc aggactctac tccctcagca gcgtgggtgac cgtgccctcc 480
154 agcagcttgg gcacccagac ctacacctgc aacgtgaatc acaagcccag caacaccaag 540
156 gtggacaaga gagttgagct caaaacccca cttggtgaca caactcacac atgccacagg 600
158 tgcccagagc ccaaatcttg tgacacacct ccccggtgcc cacggtgcc 650
161 <210> SEQ ID NO: 6
162 <211> LENGTH: 705
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial sequence ✓
166 <220> FEATURE:

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167 <223> OTHER INFORMATION: Germline Ig Gamma 4 probe ✓
 169 <400> SEQUENCE: 6
 170 ggccagcacc acatggaagc ccaagcggag ccagcacggg ggaggtgggc agccttcagg 60
 172 cactgatgcc caccagtgcc gagacgacgg ggaccgtggg caggggcttc caagccaaca 120
 174 gggcaggaca caccagaggc tgactgaggc ctccaggacg accgggctgg gagcacgagg 180
 176 aacatgacgg gatgcggcag aaccggccgt ggggtgatgc caggatgggc acgaccgacc 240
 178 tgagctcagg aggcagcaga gcgagggagg aggagaggcc ccaggtgaac ggaggggctt 300
 180 gtccaggccg gcagcatcac cagagcccag ggcagggtca gcagagctgg ccgtagggcc 360
 182 ctctctcag ccaggaccaa ggacagcagc ttccaccaag ggcccatccg tcttccccct 420
 184 ggcgccctgc tccaggagca cctccgagag cacagccgcc ctgggctgcc tggtaagga 480
 186 ctacttcccc gaaccgggtg cgggtgctgt gaactcaggc gccctgacca gcggcgtgca 540
 188 caccttcccc gctgtcctac agtctcagg actctactcc ctacgacgag tggtagccgt 600
 190 gccctccagc agcttgggca cgaagaccta cacctgcaac gtagatcaca agcccagcaa 660
 192 caccaaggtg gacaagagag ttgagtccaa atatggtccc ccgtc 705
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 196 <211> LENGTH: 399
 197 <212> TYPE: DNA
 198 <213> ORGANISM: Artificial sequence ✓
 200 <220> FEATURE:
 201 <223> OTHER INFORMATION: Germline Ig Alpha-1 probe ✓
 203 <400> SEQUENCE: 7
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 206 ccgtgagggt ggacctgcca tgagggcctg cagcccgagg gccgcccact cagcactgcg 120
 208 ggccctccag cagcctgacc agcatccccg accagcccca aggtcttccc gctgagcctc 180
 210 tgcagcacc agccagatgg gaacgtggtc atcgccctgcc tggtagcagg cttcttcccc 240
 212 caggagccac tcagtgtgac ctggagcgaa agcggacagg gcgtgaccgc cagaaacttc 300
 214 ccacccagcc aggatgcctc cggggacctg tacaccacga gcagccagct gaccctgccg 360
 216 gccacacagt gcctagccgg caagtccgtg acatgccac 399
 219 <210> SEQ ID NO: 8
 220 <211> LENGTH: 430
 221 <212> TYPE: DNA
 222 <213> ORGANISM: Artificial sequence ✓
 224 <220> FEATURE:
 225 <223> OTHER INFORMATION: Germline Ig Alpha-2 probe ✓
 227 <400> SEQUENCE: 8
 228 ctctgctaag gacagacggc catcaaggca ggacctgggc cgggccaggg ctccctcccc 60
 230 acagcagccc tcttggcagg cagccagacg cccgtgaggg tggacctgcc atgagggcct 120
 232 gcacgcggga ggccgcccac tcagcactgc gggccctcca gcagcctgac cagcatcccc 180
 234 gaccagcccc aaggtcttcc cgtgagcct cgacagcacc cccaagatg ggaacgtggt 240
 236 cgtgcgatgc ctggtagcgg gcttcttccc ccaggagcca ctacgtgtga cctggagcga 300
 238 aagcggacag aacgtgaccg ccagaaactt cccacctagc caggatgcct ccggggacct 360
 240 gtacaccacg agcagccagc tgacctgcc ggccacacag tgcccagacg gcaagtccgt 420
 242 gacatgccac 430
 245 <210> SEQ ID NO: 9
 246 <211> LENGTH: 202
 247 <212> TYPE: DNA
 248 <213> ORGANISM: Artificial sequence ✓
 250 <220> FEATURE:
 251 <223> OTHER INFORMATION: Germline Ig Epsilon probe ✓

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253 <400> SEQUENCE: 9
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256 ggaacccgac agggagccgg acgggccaca ccatccacag gcaccaaagtg gacgacccgg      120
258 cgcttcagcc tccacacaga gcccatccgt ctcccccttg acccgctgct gcaaaaacat      180
260 tccctccaat gccacctccg tg                                          202
263 <210> SEQ ID NO: 10
264 <211> LENGTH: 370
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial sequence ✓
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Germline Ig Gamma 1 probe ✓
271 <400> SEQUENCE: 10
272 acacaccaga ggctgactga ggcctccagg acgaccgggc tgggagcagc aggaacatga      60
274 ctggatgcgg cagagccggc cgtgggggtga tgccaggatg ggcacgaccg acctgagctc      120
276 aggaggcagc agagcgaggg aggaggagag gccccagggtg aacggagggg cttgtccagg      180
278 ccggcagcat caccggagcc cagggcaggg tcagcagtgc tggccgtggg gccctcctct      240
280 cagccaggac caaggacagc agcctccacc aaggggccat cgggtcttccc cctggcaccg      300
282 tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc      360
284 cccgaaccgg                                          370
287 <210> SEQ ID NO: 11
288 <211> LENGTH: 387
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial sequence ✓
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Germline Ig Gamma 2 proble ✓
295 <400> SEQUENCE: 11
296 ccaagccaac agggcaggac acaccagagg ctgactgagg cctccatgac gaccaggctg      60
298 ggagcacgag gaacatgacg ggatgcggca gagccggccg tggggtgatg ccagcatggg      120
300 caggaccac ctgagctgag gaggcagtag aacgagggag gaggagaggc cccaggtgaa      180
302 cggaggggct tgtccaggcc agcagcatca ctggagccca gggcagggtc agcagtgtctg      240
304 gccgtggggc cctctctcag ccaggacca ggacagcagc ctccaccaag ggcccatcgg      300
306 tcttccccct ggcgcctgc tccaggagca cctccgagag cacagcggcc ctgggctgcc      360
308 tggtaagga ctacttcccc gaaccgg                                          387
311 <210> SEQ ID NO: 12
312 <211> LENGTH: 391
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial sequence ✓
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Germline Ig Gamma 3 probe ✓
319 <400> SEQUENCE: 12
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324 aggagggcagc agagagaggg aggaggagag gccccagggtg aacggagggg cttgtccagg      180
326 ccggcagcat caccggagcc cagggcaggg tcagcagagc tggccgtagg gccctcctct      240
328 cagccaggac caaggacagc agcttccacc aaggggccat cgggtcttccc cctggcggcc      300
330 tgcctccagga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc      360
332 cccgaaccgg tgacgggtgc gtggaactca g                                          391
335 <210> SEQ ID NO: 13
336 <211> LENGTH: 497

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337 <212> TYPE: DNA
 338 <213> ORGANISM: Artificial sequence ✓
 340 <220> FEATURE:
 341 <223> OTHER INFORMATION: Germline Ig Gamma 4 probe ✓
 343 <400> SEQUENCE: 13
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 346 cactgatgcc caccagtgct gagacgacgg ggaccgtggg caggggcttc caagccaaca 120
 348 gggcaggaca caccagaggg tgactgaggg ctccaggacg accgggctgg gagcacgagg 180
 350 aacatgacgg gatgcggcag aaccggccgt ggggtgatgc caggatgggc acgaccgacc 240
 352 tgagctcagg aggcagcaga gcgagggagg aggagaggcc ccaggtgaac ggaggggctt 300
 354 gtccaggccg gcagcatcac cagagcccag ggcagggtca gcagagctgg ccgtagggcc 360
 356 ctctctcag ccaggaccaa ggacagcagc ttccaccaag ggcccatccg tcttcccctt 420
 358 ggcgcctgc tccaggagca cctccgagag cacagccgcc ctgggctgcc tggtaagga 480
 360 ctacttcccc gaaccgg 497
 363 <210> SEQ ID NO: 14
 364 <211> LENGTH: 61
 365 <212> TYPE: PRT
 366 <213> ORGANISM: Artificial sequence ✓
 368 <220> FEATURE:
 369 <223> OTHER INFORMATION: preferred coiled-coil presentation structure ✓
 371 <400> SEQUENCE: 14
 373 Met Gly Cys Ala Ala Leu Glu Ser Glu Val Ser Ala Leu Glu Ser Glu
 374 1 5 10 15
 377 Val Ala Ser Leu Glu Ser Glu Val Ala Ala Leu Gly Arg Gly Asp Met
 378 20 25 30
 381 Pro Leu Ala Ala Val Lys Ser Lys Leu Ser Ala Val Lys Ser Lys Leu
 382 35 40 45
 385 Ala Ser Val Lys Ser Lys Leu Ala Ala Cys Gly Pro Pro
 386 50 55 60
 389 <210> SEQ ID NO: 15
 390 <211> LENGTH: 6
 391 <212> TYPE: PRT ✓
 392 <213> ORGANISM: Artificial sequence ✓
 394 <220> FEATURE:
 395 <223> OTHER INFORMATION: loop structure ✓
 397 <400> SEQUENCE: 15
 399 Gly Arg Gly Asp Met Pro
 400 1 5
 403 <210> SEQ ID NO: 16
 404 <211> LENGTH: 69
 405 <212> TYPE: PRT
 406 <213> ORGANISM: Artificial sequence ✓
 408 <220> FEATURE:
 409 <223> OTHER INFORMATION: preferred minobody presentation structure ✓
 411 <400> SEQUENCE: 16
 413 Met Gly Arg Asn Ser Gln Ala Thr Ser Gly Phe Thr Phe Ser His Phe
 414 1 5 10 15
 417 Tyr Met Glu Trp Val Arg Gly Gly Glu Tyr Ile Ala Ala Ser Arg His
 418 20 25 30

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22